

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 11, 2006, 00:04:17 ; Search time 76 Seconds  
 Perfect score: 85 (without alignment)  
 Sequence: 1 MRYMIGLALLAAVCSAA 18

Title: US-10-031-008-7  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
 Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$  
 Maximum Match 0\$  
 Listing first 45 summaries

Database : A\_Geneseq\_21:  
 1: geneseqp1980s: \*  
 2: geneseqp1990s: \*  
 3: geneseqp2000s: \*  
 4: geneseqp2010s: \*  
 5: geneseqp2002s: \*  
 6: geneseqp2003s: \*  
 7: geneseqp2003bs: \*  
 8: geneseqp2004s: \*  
 9: geneseqp2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	18	AAB49510	Aab49510 Adenoviru
2	85	100.0	18	ABB79304	Abb79304 E3/19K si
3	85	100.0	18	ABU87174	Abu87174 Adenoviru
4	85	100.0	18	ADN00612	Adn00612 E3/19K si
5	85	100.0	18	ADO55472	Ado55472 Murine E3
6	85	100.0	18	ADO43914	Ado43914 Amino aci
7	85	100.0	27	AAR63153	Aar63153 PLA tumou
8	85	100.0	27	AAY05400	Aay05400 T-cell Be
9	85	100.0	28	AARW81051	Aaw81051 Signal pe
10	85	100.0	48	ABU87179	Abu87179 Expresshydr
11	85	100.0	56	ABU87178	Abu87178 Carbohydr
12	85	100.0	90	AYY44364	Ayy44364 KDEL rece
13	85	100.0	109	AYY44963	Aay44963 KDEL rece
14	85	100.0	109	AYY44965	Aay44965 KDEL rece
15	85	100.0	109	AYY44966	Aay44966 KDEL rece
16	82	96.5	26	ADA37032	Ada37032 Adenoviru
17	82	96.5	26	ADA37037	Ada37037 Minigene
18	81	95.3	17	AAR63147	Aar63147 Adenoviru
19	81	95.3	17	AAWB1046	Aawb1046 Signal pe
20	81	95.3	17	AYY67363	Ayy67363 Sorting s
21	81	95.3	27	AAW81049	Aaw81049 Signal pe
22	80	94.1	31	AAB35489	Aab35489 Internali
23	80	94.1	31	ADA88894	Ada88894 Internali
24	76	89.4	17	AAW81048	Aaw81048 Signal pe

## ALIGNMENTS

RESULT 1  
 ID AAB49610 standard; peptide, 18 AA.  
 XX  
 AC AAB49610;  
 XX DT 02-MAR-2001 (first entry)

XX Adenovirus B19 signal peptide sequence.  
 XX DB 02-MAR-2001  
 XX KW Antiangiogenic protein; viral particle; antitumour; pulmonary; cyostatic; antidiabetic; antirheumatic; tumour; angiogenesis; metastasis; rheumatic disease; diabetic neovascularisation; haemopoiesis; wound healing; adenovirus; signal sequence.

XX Matadenovirus.

XX OS WO200066379-A1.

XX PN WO200066379-A1.

XX PD 16-NOV-2000.

XX XX  
 PF 05-MAY-2000; 2000WHO-US012392.  
 PR 07-MAY-1999; 99US-0113243P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES .  
 XX PI Libutti SK, Feldman A;  
 XX XX DR WPI; 2001-016095/02.  
 XX PS Claim 22; Page 54; 78pp; English.

XX This invention relates to a compound comprising a recombinant nucleic acid sequence encoding an antiangiogenic protein (e.g. endostatin) inserted within a viral nucleic acid sequence. The recombinant nucleic acid sequence is packaged in a virus particle the expression of which results in the production of the antiangiogenic protein. The compound has antitumour; pulmonary; cytostatic; antidiabetic; and antirheumatic activity. The compound is useful for expressing an antiangiogenic protein in a cell to treat a tumour. The compounds can also be used for treating any disease or process mediated by angiogenesis such as leukaemia, metastasis, rheumatic diseases, diabetic neovascularisation, CC

CC haemopoiesis and wound healing. The present sequence represents an  
 CC Adenovirus E19 signal peptide. DNA encoding the peptide is used to direct  
 CC expression of the antiangiogenic protein in cells containing the compound  
 XX of the invention

SQ Sequence 18 AA;

Query Match Score 85; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db ABB79904 standard; peptide: 18 AA.

XX ABB79904 standard; peptide: 18 AA.

AC ABB79904 standard; peptide: 18 AA.

XX 05-DEC-2002 (first entry)

DE E3/19K signal peptide.

XX Endostatin; mouse; ophthalmological; ocular neovascularisation;

KW choroidal neovascularisation; gene therapy; adenovirus; vector;

KW signal peptide.

XX Mus musculus.

XX WO200257971-A2.

PN 06-SEP-2002.

PD 21-FEB-2002; 2002WO-US005316.

PR 22-FEB-2001; 2001US-0570787P.

PR 04-APR-2001; 2001US-0281296P.

XX (NOVS ) NOVARTIS AG.

XX Brazzell RK, Campochiaro PA, Dixon KH;

PS DR; 2002-698636/75.

XX Example 1; Page 19; 44pp; English.

XX Treating or preventing choroidal neovascularization comprises increasing

CC the amount of endostatin in ocular tissues of afflicted individuals to a  
 PR choroidal neovascularization inhibiting level.

XX PS Example 1; Page 19; 44pp; English.

XX The present sequence is that of the 18-amino acid E3/19K signal peptide.

CC A nucleic acid encoding this signal peptide was inserted upstream of a  
 CC murine endostatin coding sequence in the construction of an adenovirus

CC vector. The viral vector was used to infect murine colon adenocarcinoma

CC MCF7 cells for production of endostatin. A claimed method for the

CC treatment of ocular, especially choroidal, neovascularisation involves

CC increasing the level of endostatin in ocular tissue, especially the level

CC of human endostatin (see ABB79901). The increase is effected by

CC administering viral vector, especially an adenovirus, adeno-associated

CC virus, a retrovirus or lentivirus vector, comprising an endostatin-

CC encoding nucleic acid. Cells secreting endostatin may be encapsulated and

CC implanted within an individual

XX SQ Sequence 18 AA;

Query Match Score 85; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRYMILGILAAVCSAA 18

|||||||  
 1 MRYMILGILAAVCSAA 18

RESULT 3  
 ABU87174 standard; peptide: 18 AA.  
 XX ID ABU87174  
 AC ABU87174;  
 XX DT 23-OCT-2003 (revised)  
 XX DT 03-JUL-2003 (first entry)  
 XX DS Adenovirus E3 leader sequence.  
 XX KW Carbohydrate antigen; mimotype; vaccine; infection; tumour; pathogen;  
 XX KW cytosstatic; antibacterial; antigen; E3 leader sequence.  
 XX OS unidentified adenovirus.  
 XX US2003017197-A1.  
 PN XX 23-JAN-2003.  
 PD XX 28-JUN-2001; 2001US-00894594.  
 XX PR 04-FEB-1998;  
 XX PR 04-FEB-1999;  
 XX PR 28-JUN-2000; 2000US-0214517P.  
 XX PR 07-NOV-2000; 2000US-00601558.  
 XX PA (KIEBER / KLEBER-EMMONS T.  
 PA (WEINER / WEINER D B.  
 PA (MONZ / MONZAVI-KARBASSI B;  
 XX PI Kieber-Emmons T, Weiner DB, Monzavi-Karbassi B;  
 XX DR WPI; 2003-401670/38.  
 XX PR Preparing a recombinant antibody or peptide that mimics an antigenic  
 PR carbohydrate, for generating an immune response against a pathogen,  
 PR comprises identifying a peptide sequence that is cross reactive with an  
 PR antigenic carbohydrate.

XX Example 9; Page 20; 75pp; English.

XX The invention relates to preparing a recombinant antibody or a peptide  
 CC that mimics an antigenic carbohydrate comprising identifying a peptide  
 CC sequence that is immunogenically cross reactive with an antigenic  
 CC carbohydrate, and synthesising a recombinant antibody comprising the  
 CC peptide sequence or a peptide comprising at least two repeating units of  
 CC the peptide sequence. Also included are a method of generating an immune  
 CC response against a pathogen or tumour cell in an individual (comprising  
 CC the invention), a method of enhancing binding of anti-antigenic  
 CC carbohydrate antibodies to the antigenic carbohydrate in an individual  
 CC (comprising administering to the individual the carbohydrate antigen peptide  
 CC or antibody above, a DNA vaccine, live attenuated vaccine or recombinant  
 CC vaccine comprising a nucleic acid sequence that encodes then peptides of  
 CC the invention), a method of enhancing binding of anti-antigenic  
 CC carbohydrate antibodies to the antigenic carbohydrate in an individual  
 CC (comprising administering to the individual anti-anti-antigenic carbohydrate  
 CC antibodies and a peptide comprising 1-3 repeat units of a peptide  
 CC sequence that mimics an antigenic carbohydrate), a method of inhibiting  
 CC binding of a ligand to a receptor that is an antigenic carbohydrate using  
 CC the peptides/antibodies of the invention and a method of identifying  
 CC peptide sequences that can induce an immune response against two or more  
 CC different pathogens (comprising identifying a peptide sequence that is  
 CC immunogenically cross reactive with an antigenic carbohydrate, which is  
 CC associated with a pathogen, administering a peptide comprising the  
 CC peptide sequence to an animal to induce an immune response and analysing  
 CC the immune response to identify two or more pathogens against which the  
 CC immune response cross reacts. The peptides, antibodies and methods are  
 CC useful for generating a prophylactic or therapeutic immune response  
 CC against a tumour cell or a pathogen in an individual. The peptides are  
 CC useful as immunogenic agents, vaccines, adjuvants, enhancers of antibody



Db	1	MRYMILGLLAAAVCSAA	18		Query Match Score 85; DB 8; Length 18;
RESULT 6				Best Local Similarity 100.0%; Pred. No. 2.4e-06;	Mismatches 0; Indels 0; Gaps 0;
ADO43914	ID	ADO43914 standard	peptide, 18 AA.		
XX					
AC	ADO43914;				
XX					
DT	15-JUL-2004	(first entry)			
XX					
DB	Amino acid sequence of the E3/19K signal peptide.				
XX					
KW	retina; endostatin; vascular endothelial growth factor receptor;				
KW	plasmaminogen fragment; angiostatin; plasmaminogen fragment;				
KW	rod-derived cone viability factor; antiangiogenic antithrombin;				
KW	cartilage-derived inhibitor; CD59 complement fragment;				
KW	fibronectin fragment; Gro-beta, heparanase; chorionic gonadotropin;				
KW	interferon; interferon inducible protein; IP-10; interleukin-12;				
KW	kringle 5; metalloprotease inhibitor; Placental ribonuclease inhibitor;				
KW	plasminogen activator inhibitor; platelet factor-4; PRP; prolactin;				
KW	proliferin-related protein; PRP; thrombospondin-1; TSP-1;				
KW	transforming growth factor-beta; TGF-b; vasculostatin; vasostatin;				
KW	calreticulin; retinal disorder; retinal detachment; diabetic retinopathy;				
KW	retinal neovascularization; choroidal neovascularization; retinal edema.				
XX					
OS	unidentified adenovirus.				
XX					
PN	Synthetic.				
XX					
PD	WO2004028635-A1.				
XX					
PD	08-APR-2004.				
XX					
PP	26-SEP-2003; 2003WO-EP010725.				
XX					
PR	27-SEP-2002; 2002US-0414048P.				
XX					
PA	(NOVS ) NOVARTIS AG.				
PA	(NOVS ) NOVARTIS PHARMA GMBH.				
PI	Campochiaro PA, Kaleko M;				
XX					
DR	WPI; 2004-305131/28.				
XX					
PS	Example 1; Page 11; 47PP; English.				
XX					
CC	The specification describes a method for delivering a protein to the retina of a subject. The method comprises percutaneously injecting a viral vector comprising a nucleic acid into the subject. Alternatively, the viral vector may encode soluble vascular endothelial growth factor receptor, pigment epithelium-derived factor, angiostatin (plasminogen fragment), rod-derived cone viability factor, antiangiogenic antithrombin III, cartilage-derived inhibitor (CDI), CD59 complement fragment, fibronectin fragment, Gro-beta, a heparinase, human chorionic gonadotropin (hCG), an interferon, interferon inducible protein (IP-10), interleukin-12, kringle 5 (plasminogen fragment), metalloprotease inhibitors (TBV18), placental ribonuclease inhibitor, plasminogen activator inhibitor, platelet factor-4 (PF4), prolactin 16kD fragment, proliferrin-related protein (PRP), thrombospondin-1 (TSP-1), transforming growth factor-beta (TGF-b), vasculostatin or vasostatin (calreticulin fragment). The method is useful in treating disorders, e.g., retinal detachment, a subject for treatment of retinal disorders, e.g., retinal detachment, diabetic retinopathy, retinal neovascularization, choroidal neovascularization or retinal edema. The present signal peptide was attached to murine endostatin, and used to construct viral vectors for use in the method of the invention.				
XX	Sequence 18 AA;				
SQ	Sequence 27 AA;				
Query	1	MRYMILGLLAAAVCSAA	18	Query Match Score 85; DB 2; Length 27;	
Best Local Similarity 100.0%; Pred. No. 3.7e-06;					
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Db	1	MRYMILGLLAAAVCSAA	18		
		1	MRYMILGLLAAAVCSAA		

RESULT 8		OS Homo sapiens.
AY05400	ID AY05400 standard; peptide: 27 AA.	XX Chimeric.
	XX	Location/Qualifiers
	XX	Key 1..18
	AC	Peptide /note= "signal peptide"
	XX	Peptide 19..28
	XX	/note= "cytotoxic T cell epitope"
DT	01-JUL-1999 (first entry)	XX WO955133-A1.
DB	T-cell Beta-gal epitope with leader peptide.	XX
XX		PD 10-DEC-1998.
KW	T-cell; beta-galactosidase epitope; beta-gal; tumour growth reduction;	XX 04-JUN-1998; 98WO-US011533.
KW	recombinant influenza virus; tumour-associated antigen; vaccine;	XX 06-JUN-1997; 97US-00870341.
KW	tumour formation prevention.	XX
XX	Unidentified.	XX
OS		PA (REGC ) UNIV CALIFORNIA.
PN	WC984834-A1.	PA (TUSC-) UNIV SOUTHERN CALIFORNIA.
XX		XX Mitchell MS, Deans RJ, Minev BR, Kan-Mitchell J;
PD	05-NOV-1998.	XX WPI; 1999-080820/07.
XX		XX
PP	30-APR-1998; 98WO-US008929.	PT New MG50 melanoma associated antigen fragments - used to develop products for the detection, treatment and prevention of MG50-expressing cancers,
XX		PR e.g., melanoma, lung cancer or rhabdomyosarcoma.
PR	30-APR-1997; 97US-0045176P.	XX
XX		PS Claim 12; Page 58; 79pp; English.
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.		XX This peptide comprises a claimed cytotoxic T cell epitope composed of a signal peptide and a T cell epitope (see AW81032) derived from the human MG50 melanoma associated antigen (see AW81030). The signal peptide can facilitate presentation of the epitope as a complex with an MHC molecule at the surface of an antigen presenting cell (APC). The invention provides additional T cell epitopes (see AW81031-15) from MG50, and APCs that can express an MG50 T cell epitope complexed with an MHC molecule on their surfaces, and which can be administered to a patient having a cancer that contains MG50-expressing cells in order to stimulate an active immune response. MG50 vaccines comprising an MG50 polypeptide, a T cell epitope optionally attached to a signal peptide, an anti-idiotypeic antibody or a nucleic acid molecule encoding an MG50 polypeptide or T cell epitope can be administered for preventative or therapeutic purposes. The products and methods are used for the detection, treatment and prevention of e.g., melanoma, lung cancer and rhabdomyosarcoma
PA (USSH ) US NAT INST OF HEALTH.		XX
XX		PS Sequence 28 AA;
PI	Garcia-Sastre A, Palese P, Rosenberg SA, Reetifo NP;	XX
XX	WPI; 1999-024033/02.	Query Match Score 85; DB 2; Length 28;
DR		Best Local Similarity 10.0%; Pred. No. 3.9e-06;
XX		Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	Recombinant influenza viruses containing tumour-associated antigen sequence - inserted into a structural gene, is useful for immunising patients to reduce or prevent tumours.	Qy 1 MRYMLGLLALAAVCSAA 18
PR	Example: Fig 1; 16pp; English.	Db 1 MRYMLGLLALAAVCSAA 18
XX	This sequence represents a T-cell beta-galactosidase (beta-gal) epitope with a leader peptide. The invention relates to a recombinant influenza virus genome which contains a region encoding a tumour-associated antigen (such as this sequence). The recombinant virus is used in immunogenic formulations or vaccines for immunising tumour-bearing or tumour-free patients in order to reduce tumour growth or prevent tumour formation respectively	RESULT 10
XX	Sequence 27 AA;	ID AB087179 standard; peptide: 48 AA.
SQ	Query Match Score 85; DB 2; Length 27;	XX
	Best Local Similarity 10.0%; Pred. No. 3.7e-06;	AC ABU87179;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX DT 03-JUL-2003 (first entry)
Qy	1 MRYMLGLLALAAVCSAA 18	DE Expression vector PcdNaggi expressed protein.
Db	1 MRYMLGLLALAAVCSAA 18	XX
		KW Carbohydrate antigen; mimotope; vaccine; infection; tumour; pathogen;
		KW cyostatic; antibacterial; antigen; B3 leader sequence; HIV;
		KW T helper cell epitope.
		OS Human immunodeficiency virus 1.
		OS unidentified adenovirus.
RESULT 9		
AAW81051	ID AAW81051 standard; peptide: 28 AA.	
	XX	
AC	AC	
AAW81051;		XX
XX		DT
DT	10-MAY-1999 (first entry)	XX
XX		DE
DE	Signal peptides-cytotoxic T cell epitope fusion.	XX
XX		KW
KW	MG50; melanoma Gene-50; melanoma associated antigen; human: cancer;	KW
KW	lung cancer; rhabdomyosarcoma; diagnosis; therapy; vaccine;	KW
KW	cytotoxic T cell epitope; signal peptide.	KW
XX		OS Synthetic.
OS		





**PS Disclosure:** Fig 6; 87pp; English.

XX WPI; 2000-195296/17.

CC DR N-PSDB; AR25099.

CC The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astrocytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human cartilage oligomeric matrix protein (COMP) pentamerisation domain; a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GBCC is an alteration of rat COMP which provides increased stability via disulphide bonds. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 109 AA;

Query Match Score 85; DB 3; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLALAVALVCSAA 18

Db 1 MRYMILGLLALAVALVCSAA 18

Sequence 109 AA;

Query Match Score 85; DB 3; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLALAVALVCSAA 18

Db 1 MRYMILGLLALAVALVCSAA 18

RESULT 14  
AY44965 ID AY44965 standard; protein; 109 AA.  
XX AC AY44965;  
XX DT 12-SEP-2003 (revised)  
DT 23-MAY-2000 (first entry)  
XX KDEL receptor inhibitor protein-8.  
KW KDEL receptor inhibitor; heat shock protein; immune response;  
KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;  
KW melanoma; carcinoma; glioblastoma; astrocytoma; oncogene;  
KW infectious disease; allergy; autoimmune disease.  
OS Unidentified adenovirus; E3.  
OS Homo sapiens.  
OS Camelus sp.  
XX Key Peptide 1..20  
FT Location/Qualifiers /label= Signal peptide  
FT /note= "Derived from adenovirus E3"  
FT Domain 30..75  
FT /note= "Human TSP 3 trimersation domain"  
FT Domain 76..99  
FT /note= "Camel IgG linker domain"  
XX WO200006729-A1.  
XX 10-FEB-2000.  
XX 28-JUL-1999; 99WO-US017147.  
XX 29-JUL-1998; 98US-00124671.  
XX (SLOAN KETTERING INST CANCER RES.  
PA Rothman JE, Mayhew M, Hoe MH;

XX Disclosure; Fig 8; 87pp; English.

XX The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astrocytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human thrombospondin 3 (TSP3) trimerisation domain; a camel IgG linker domain and the carboxy-terminal sequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 109 AA;

Query Match Score 85; DB 3; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLALAVALVCSAA 18  
Db 1 MRYMILGLLALAVALVCSAA 18

RESULT 15  
AY44966 ID AY44966 standard; protein; 109 AA.  
XX AC AY44966;  
XX DT 12-SEP-2003 (revised)  
DT 23-MAY-2000 (first entry)  
XX KDEL receptor inhibitor protein-9.  
XX KDEL receptor inhibitor; heat shock protein; immune response;  
KW oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia;  
KW melanoma; carcinoma; glioblastoma; astrocytoma; oncogene;  
KW infectious disease; allergy; autoimmune disease.  
OS Unidentified adenovirus; E3.  
OS Homo sapiens.  
OS Camelus sp.  
XX Key Peptide 1..20  
FT Location/Qualifiers /label= Signal peptide  
FT /note= "Derived from adenovirus E3"  
FT Domain 30..75  
FT /note= "Human TSP4 trimersation domain"  
FT Domain 76..99  
FT /note= "Camel IgG linker domain"  
XX WO200006729-A1.  
XX 10-FEB-2000.  
XX 28-JUL-1999; 99WO-US017147.  
XX 29-JUL-1998; 98US-00124671.  
XX (SLOAN KETTERING INST CANCER RES.  
PA Rothman JE, Mayhew M, Hoe MH;

XX  
PP 28-JUL-1999; 99WO-US017147.  
XX PR 29-JUL-1998; 98US-00124671.  
XX PA (SLOK ) SLOAN KEPTERING INST CANCER RES.  
XX PI Rothman JB, Mayhew M, Hoe MH;  
XX DR WPI; 2000-185296/17.  
XX N-PSDB; AAZ20500.  
XX Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell.  
XX Disclosure: Fig 9; 87pp; English.  
XX The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astrocytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human thrombospondin 4 (TSP4) trimerisation domain, a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequent GCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 109 AA:

Query Match 100.0%; Score 85; DB 3; Length 109;  
Best Local Similarity 100.0%; Ped. No. 1.7e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Ov 1 MRYNMILGLIALAAVCSAA 18  
Db 1 MRYNMILGLIALAAVCSAA 18

Search completed: January 11, 2006, 00:08:16  
Job time : 77 secs

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hypothetical prote						
probable membrane						
probable chaperone						
probable chaperone						
hypothetical prote						
probable secreted						
Y19X protein - BSC						
secreted protein						
hypothetical prote						
iron ABC transport						
Na+/caurocholate co						
hypothetical prote						
probable large sec						
homeotic protein B						
methyl-accepting C						
Om protein - protein search, using sw model						
Run on:	January 11, 2006, 00:05:17 ; Search time 16 Seconds (without alignments) 108.244 Million cell updates/sec					
Title:	US-10-031-008-7					
Perfect score:	85					
Sequence:	MRYMILGULLAAVCSSA 18					
Score:	100.0					
Program:	psort					

Searched: 283416 seqs, 96216763 residues  
Matched number of hits containing chosen parameters.  
Gap0 10.0 ; Gapext 0.3

Total number of hits satisfying chosen parameters.

Post-processing: Minimum Match 0% Maximum Match 100%

**Database :** PIR 80 : \*  
**Listing First 45 Summaries**

```
1: p1r1:=  
2: p1r2:=*  
3: p1r3:=*
```

4: *Pi4:\**

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	159	1 Q6ADB	early B3 18.5K gly hypothetical prote
2	47	55.3	596	2 T19740	hypothetical prote
3	46	54.1	131	2 D83173	hypothetical prote
4	46	54.1	5175	2 T20992	hypothetical prote
5	46	54.1	5198	2 T43290	hemicytial precurs
6	45	52.9	160	1 ERADAS5	early B3 18.5K gly
7	45	52.9	3390	1 GNWVD3	hypothetical prote
8	44	51.8	152	2 T48227	hypothetical prote
9	44	51.8	255	2 B7522	hypothetical prote
10	44	51.8	334	2 DB7575	probable membrane
11	44	51.8	372	2 AB0276	alcohol dehydrogen
12	44	51.8	742	2 A43340	alcohol dehydrogen
13	44	51.8	742	2 JS0126	hypothetical prote
14	43.5	51.2	152	2 GB3476	hypothetical prote
15	43	50.6	64	2 T22247	osteocalcin precursor
16	43	50.6	100	1 GEBO	osteocalcin precursor
17	42	49.4	100	1 GERU	hypothetical prote
18	42	49.4	221	2 A70543	ferric enterobacti
19	42	49.4	334	2 S16296	ferric enterobacti
20	42	49.4	334	2 A85558	ferric enterobacti
21	42	49.4	334	2 B90107	ferric enterobacti
22	42	49.4	335	2 AB0575	manganese peroxidase
23	42	49.4	380	2 JC2579	probable MFS trans
24	42	49.4	408	2 BB3133	heat shock protein
25	42	49.4	417	1 A40568	heat shock protein
26	42	49.4	417	1 A44843	heat shock protein
27	42	49.4	417	1 S20608	calcium channel protein
28	42	49.4	2223	2 A4474	MG2277 homolog F11
29	41.5	48.8	887	2 ST7768	

Qy 2 RYML--GLLAAAVCS 16  
 Db 141 RYLILIGFLCLASVCS 157

RESULT 5  
 T43290 hemicentin precursor - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 C;Accession: T43290  
 C;Cross-references: UNIPARC:UPI0000110172; EMBL:AF074901; PIDN: AAC26792.

D83173 hypothetical protein PA3788 [imported] - *Pseudomonas aeruginosa* (strain PAO1)  
 C;Species: *Pseudomonas aeruginosa*  
 C;Accession: D83173  
 C;Cross-references: UNIPARC:UPI0000005B13; GB:AE004091; NID: 10984043  
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brandom, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen  
 A;Reference number: A82950; MUID:20437337; PMID:10984043  
 A;Accession: D83173  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-131 <SPO>  
 A;Cross-references: UNIPROT:Q9HKX7; UNIPARC:UPI0000005B13; GB:AE004091; NID: 10984043  
 A;Experimental source: strain PAO1  
 C;Genetics:  
 A;Gene: PA3788

Query Match Score 46; DB 2; Length 131;  
 Best Local Similarity 56.2%; Pred. No. 7.3%;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RYMLGLLAAVCSA 17  
 Db 70 RYLILIGFLCLASVCS 85

RESULT 4  
 T20992 hypothetical protein F15G9.4a - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Accession: T20992  
 C;Cross-references: UNIPARC:T24733  
 R;Sulston, J.  
 submitted to the EMBL Data Library, December 1994  
 A;Reference number: Z19355  
 A;Accession: T20992  
 A;Status: Preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-5198 <WIL>  
 A;Cross-references: UNIPARC:UPI0000110172; EMBL:247068; PIDN:CAA87335.1; GSPDB:GN00028;  
 A;Experimental source: Clone T09B9  
 C;Genetics:  
 A;Gene: him-4; F15G9.4b  
 A;Map position: X  
 A;Intervall: 85/1..120/1; 334/3..370/1; 477/2..606/3; 664/1..935/3; 977/1..1051/3; 1184/3;  
 A;Accession: T24734  
 A;Status: Preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-5198 <WIL2>  
 A;Cross-references: UNIPARC:UPI0000110172; EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028;

Query Match Score 46; DB 2; Length 5198;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 YMIGLGLLAAVCSA 17  
 Db 9 YGVIGLGLLATTCS 23

RESULT 6  
 ERADAS  
 early E3 18.5K glycoprotein - human adenovirus 5  
 C;Species: Mastadenovirus hs (human adenovirus 5)  
 A;Note: host Homo sapiens (man)  
 C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
 C;Accession: A03822; A22515  
 R;Cladaras, C.; Wold, W.S.M.  
 Virology 140, 28-43, 1985  
 A;Title: DNA sequence of the early E3 transcription unit of adenovirus 5.  
 A;Reference number: A94335; MUID:85092388; PMID:2981456  
 A;Accession: A03822  
 A;Molecule type: DNA  
 A;Residues: 1-160 <CIA>  
 R;Wold, W.S.M.; Cladaras, C.; Deutscher, S.L.; Kapoor, Q.S.  
 J. Biol. Chem. 260, 2424-2431, 1985  
 A;Title: The 19-kDa glycoprotein coded by region B3 of adenovirus 5.  
 A;Reference number: A22515  
 A;Accession: A22515  
 A;Molecule type: DNA  
 A;Residues: 1-160 <WOL>

Query Match Score 46; DB 2; Length 5175;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 YMIGLGLLAAVCSA 17  
 Db 9 YGVIGLGLLATTCS 23

A;Cross-references: UNIPARC:UPI0000129AE7; GB:MI2406; PIDN:g209911; PID:AAA42492.1; PID: A;Status: preliminary  
 C;Superfamily: adenovirus early B3 18.5K glycoprotein, transmembrane protein  
 C;Keywords: early protein; Glycoprotein (covalent) #status predicted  
 P:30,79/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.9%; Score 45; DB 1; Length 160;  
 Best Local Similarity 69.2%; Pred. No. 12;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 A;Map position: 5  
 A;Introns: 44/2; 8/3  
 A;Note: T7H20.11.0

Qy 1 MRYMLGLIALAA 13  
 :||:|||:|||:  
 Db 2 IRYIILGLILLAS 14

RESULT 7  
 GRWVD3 genome polyprotein - dengue virus type 3  
 N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS5  
 a; nonstructural protein NSab; nonstructural protein NS5  
 C;Species: dengue virus type 3  
 C;Accession: A34774  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 31-Dec-2004  
 R;Osatomi, K.; Sumiyoshi, H.  
 Virology 176, 643-647, 1990.  
 A;Title: Complete nucleotide sequence of dengue type 3 virus genome RNA.  
 A;Reference number: A34774; PMID:90266483; PMID:2345967  
 A;Accession: A34774  
 A;Molecule type: genomic RNA  
 A;Residues: 1-3390 <OSA>  
 A;Cross-references: UNIPROT:P27915; UNIPARC:UPI0000131DFE; GB:MR93130; NID:g32346B; PIDN:  
 C;Superfamily: hepatitis C virus genome polyprotein  
 C;Keywords: capsid protein; envelope protein; glycoprotein; nonstructural protein;  
 P:1-114/Product: capsid protein #status predicted <SAP>  
 P:16-67/Domain: transmembrane #status predicted <TM1>  
 P:115-280/Product: membrane protein precursor #status predicted <MBP>  
 P:115-205/Domain: non-terminal signal sequence #status predicted <SIG>  
 P:206-280/Product: membrane protein #status predicted <MEN>  
 P:266-280/Domain: transmembrane #status predicted <TM3>  
 P:281-73/Product: envelope protein #status predicted <ENV>  
 P:724-746/Domain: transmembrane #status predicted <TM4>  
 P:753-771/Domain: transmembrane #status predicted <TM5>  
 P:774-1184/Domain: nonstructural protein NS1 #status predicted <NS1>  
 P:1156-1175/Domain: transmembrane #status predicted <TM6>  
 P:1185-1343/Product: nonstructural protein NS2 #status predicted <N2A>  
 P:1344-1433/Product: nonstructural protein NS2B #status predicted <N2B>  
 P:1474-2092/Product: nonstructural protein NS3 #status predicted <NS3>  
 P:1667-1674/Region: nucleotide-binding motif A (P-loop) predicted B  
 P:1754-1759/Region: nucleotide-binding motif B  
 P:1758-1761/Region: DEAH motif  
 P:2093-3378/Product: nonstructural protein NS4a #status predicted <N4A>  
 P:2379-2490/Product: nonstructural protein NS4b #status predicted <N4B>  
 P:2491-3390/Product: nonstructural protein NS5 #status predicted <NS5>  
 P:183,347,433,750,903,980,1132,1188,1661,2300,2304,2386,2456,2702,2712/Binding site: car

Query Match 52.9%; Score 45; DB 1; Length 3390;  
 Best Local Similarity 41.2%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 A;Map position: 5  
 A;Introns: 44/2; 8/3  
 A;Note: T7H20.11.0

Qy 1 MRYMLGLIALAAVCSA 17  
 :||:|||:|||:  
 Db 2226 LAYVVGILTLAAIVAA 2242

RESULT 8  
 T48227 hypothetical protein T7H20.110 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 R;Bayan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mex  
 Submitted to the Protein Sequence Database, March 2000  
 A;Reference number: Z24488  
 A;Accession: T48227

Query Match 51.8%; Score 44; DB 2; Length 334;  
 Best Local Similarity 50.0%; Pred. No. 30;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

3 YMIGLGLAAVCSAA 18  
 : ||| : | | | |  
 9 FVALGIMAMLMACSPA 24

RESULT 11  
 AB0276 probable membrane protein YPO2266 [imported] - *Yersinia pestis* (strain C932)  
 C;Species: *Yersinia pestis*  
 C;Accession: AB0276  
 C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 R;Parbhoo, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; den-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skellam, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: AB0276  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-372 <KUR>  
 A;Cross-references: UNIPROT:Q8ZEB5; UNIPARC:UPI00000CD8C9; GB:AL590842; PIDN:CAC91070.1;  
 C;Genetics:  
 C;Superfamily: probable antibiotic resistance protein YybfF  
 C;Gene: YP02266  
 C;Genetics:  
 C;Superfamily: probable antibiotic resistance protein YybfF  
 Query Match Score 44; DB 2; Length 372;  
 Best Local Similarity 51.8%; Pred. No. 32;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 4 MIIGLGLAAVC 15  
 : ||| : | | | |  
 Db 206 LVIGLFLAAAC 217

RESULT 12  
 A49340 alcohol dehydrogenase (EC 1.1.1.-) precursor - *Acetobacter pasteurianus* (strain NCI1380)  
 C;Species: *Acetobacter pasteurianus*  
 C;Accession: A49340  
 C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 05-Oct-2004  
 R;Takemura, H.; Kondo, K.; Horinouchi, S.; Beppu, T.  
 J;Bacteriol. 175, 6857-6866, 1993  
 A;Title: Induction by ethanol of alcohol dehydrogenase activity in *Acetobacter pasteurianus*  
 A;Reference number: A49340; MUID:94042848; PMID:8226628  
 A;Accession: A49340  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-742 <TAK>  
 A;Cross-references: UNIPROT:Q53362; UNIPARC:UPI00000BDEED; GB:D13893; NID:9517067; PIDN:  
 C;Keywords: glucose/alcohol /shikimate dehydrogenase  
 C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match Score 44; DB 2; Length 742;  
 Best Local Similarity 47.1%; Pred. No. 54;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 RYMIGLGLAAVCSAA 18  
 : ||| : | | | |  
 Db 9 RRSLLGTLAACTICAAA 25

RESULT 13  
 JS0326 alcohol dehydrogenase (EC 1.1.1.-) 72K chain precursor - *Acetobacter aceti*  
 C;Species: *Acetobacter aceti*  
 C;Accession: JS0326  
 C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 05-Oct-2004  
 R;Inoue, T.; Sunagawa, M.; Mori, A.; Imai, C.; Fukuda, M.; Takagi, M.; Yano, K.  
 J;Bacteriol. 171, 3115-3122, 1989  
 A;Title: Cloning and sequencing of the gene encoding the 72-kilodalton dehydrogenase subunit  
 A;Reference number: JS0326; MUID:8925070; PMID:2722742  
 A;Accession: JS0326

A;Molecule type: DNA  
 A;Residues: 1-742 <INO>  
 A;Cross-references: UNIPROT:PA8278; UNIPARC:UPI000012930E; GB:D90004; GB:D9033  
 A;Experimental source: strain K6033  
 A;Note: amino terminal of mature protein is confirmed  
 C;Genetics:  
 A;Gene: adbl  
 C;Superfamily: glucose/alcohol /shikimate dehydrogenase  
 C;Keywords: alcohol metabolism; NAD; oxidoreductase  
 F;1-75/Domain: signal sequence #status predicted <SIG>  
 F;36-742/Product: alcohol dehydrogenase 72K dehydrogenase chain #status predicted <ADC>  
 Query Match Score 44; DB 2; Length 742;  
 Best Local Similarity 47.1%; Pred. No. 54;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 Qy 2 RYMIGLGLAAVCSAA 18  
 : ||| : | | | |  
 Db 9 RRSLLGTLAACTICAAA 25

RESULT 14  
 G83476 hypothetical protein PA1343 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
 C;Species: *Pseudomonas aeruginosa*  
 C;Accession: G83476  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Britton, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
 A;Reference number: A82950; MUID:10984043  
 A;Accession: G83476  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-152 <STO>  
 A;Cross-references: UNIPROT:Q9I401; UNIPARC:UPI00000C5326; GB:AE004564; GB:AE004091; NID:9517067  
 A;Experimental source: strain PA01  
 C;Genetics:  
 A;Gene: PA1343

Query Match Score 43.5%; DB 2; Length 152;  
 Best Local Similarity 68.4%; Pred. No. 19;  
 Matches 13; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 MRYYMLGLLA-LAAVCSAA 18  
 : ||| : | | | | | | | |  
 Db 1 MRYYLISLLAVIAAPAWAA 19

RESULT 15  
 T25247 hypothetical protein T24F1.5 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Accession: T25247  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 R;Chui, C.  
 submitted to the EMBL Data Library, June 1995  
 A;Reference number: Z20004  
 A;Accession: T25247  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-64 <WIL>  
 A;Cross-references: UNIPROT:Q22746; UNIPARC:UPI0000076473; EMBL:249912; PIDN:CAA90139-1,  
 C;Genetic:  
 A;Gene: CEP:T24F1.5  
 A;Map position: 2  
 A;Introns: 33/1  
 Query Match Score 43%; DB 2; Length 64;  
 Best Local Similarity 52.9%; Pred. No. 12;

	Matches	9;	Conservative	3;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	MRVMILGILAAVCSA	17	:            :						
Db	1	MRPVLALALVLPATOA	17							

Search completed: January 11, 2006, 00:10:05  
Job time : 17 secs

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OM protein - protein search, using SW model

Run on: January 11, 2006, 00:04:42 ; Search time 71 Seconds  
(without alignments)

178.866 Million cell updates/sec

Title: US-10-031-008-7

Perfect score: 85

Sequence: I MRYMTIGLILAAVCSAA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs., 705528306 residues

Total number of hits satisfying chosen parameters:

2166443

Description

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 05\_80:  
 1: uniprot\_sprot:  
 2: uniprot\_trembl:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	85	100.0	159	E3GL_ADE02
2	85	100.0	159	E3GL_ADE06
3	85	100.0	159	O91024 ADR02
4	85	100.0	159	Q779F5_ADE02
5	64	75.3	160	O12399_ADR01
6	54	63.5	81	Q75WH5_MACGS
7	51	60.0	179	Q9SP73_HAEIR
8	51	60.0	208	Q7QID4_ANOPHELES
9	51	60.0	294	Q76KU1_SYNPKA
10	49	57.6	110	Q5FP07_GLICK
11	49	57.6	294	Q4USU3_XANCP
12	49	57.6	294	Q8PB18_STRAW
13	48	56.5	181	Q9V5Z3_DROME
14	48	56.5	188	Q95T42_DROME
15	48	56.5	250	Q5U195_DROME
16	48	56.5	490	Q9VLV5_DROME
17	48	56.5	557	QSNR85_ZYMO
18	47.5	55.9	135	1_TLS_CAVPO
19	47	55.3	466	Q18472_CAEEL
20	47	55.3	471	Q5AXY5_EMENTI
21	47	55.3	646	Q6YT52_ORYZA
22	47	55.3	647	Q84ZH7_ORVSA
23	46	54.1	131	Q9HXXK7_PSEAB
24	46	54.1	140	Q82PUI_STRAW
25	46	54.1	310	Q8MVK4_9ASCI
26	46	54.1	455	Q8G7J6_BIFLO
27	46	54.1	523	Q9V1Y4_DROME
28	46	54.1	595	Q4V5Q7_DROME
29	46	54.1	1895	Q7R599_GIALLA
30	46	54.1	2258	1_POL1_BAMMN
31	46	54.1	2258	055455_9POTY

## ALIGNMENTS

RESULT 1		PRT;		159 AA..	
ID	E3GL_ADE02	STANDARD;			
AC	P68978	P032511;			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	10-MAY-2005	(Rel. 47, Last annotation update)			
DB	Early B3 18.5	kDa glycoprotein precursor (GP19K)	(E3-19K)	(E3-19K)	(E3gp 19-
DB	kDa) (B19).				-kDa)
OS	Human adenovirus 2 (HAdV-2)	viruses; no RNA stage;	Adenoviridae; Mastadenovirus.		
OC					
NCBI_TaxID	10515;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE:810103687; PubMed:6253880;				
RA	Herisse J., Courtois G., Galibert F.;				
RT	"Nucleotide sequence of the E201 fragment of adenovirus 2 genome.";				
RL	Nucleic Acids Res. 8:2173-2192 (1980).				
RN	[2]				
RP	PROTEIN SEQUENCE OF N-TERMINUS, AND N-GLYCOSYLATION.				
RX	MEDLINE:85110985; PubMed:31882694;				
RA	Wold W.S.M., Cladaras C., Kapoor Q.S.;				
RT	"The 19-kDa glycoprotein coded by region B3 of adenovirus.				
RL	Purification, characterization, and structural analysis."				
RN	[3]				
RP	DISULFIDE BONDS, AND MUTAGENESIS OF CYS-28; CYS-39; CYS-45; CYT-100;				
RA	Wold W.S.M., Cladaras C., Deutscher S.L., Kapoor Q.S.;				
RT	"Nucleotide sequence of the E201 fragment of adenovirus.				
RL	Purification, characterization, and structural analysis."				
RX	CYS-118; CYS-126 AND CYS-139.				
RA	Sester M., Burger H.-G.;				
RT	"Conserved cysteine residues within the E3/19K protein of adenovirus type 2 are essential for binding to major histocompatibility complex RT antigens."				
RT	J. Virol. 68:5423-5432 (1994).				
CC	-1- FUNCTION: Binds and retains class I heavy chains in the endoplasmic reticulum during the early period of virus infection, thereby impairing their transport to the cell surface. Also delays the expression of class I alleles that it cannot affect by direct retention.				
CC	Binds transporters associated with antigen processing (TAP) and acts as a tapasin inhibitor, preventing class I/TAP association. In consequence, infected cells are masked for immune recognition by cytotoxic T lymphocytes (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic reticulum.				
CC	-1- DEVELOPMENTAL STAGE: Expressed at early period of virus infection.				
CC	-1- DOMAIN: The luminal domain binds directly to the peptide-binding domain of class I molecules.				
CC	-1- PTM: Both disulfide bonds are absolutely critical for the interaction with MHC antigens.				
CC	-1- PTM: N-Glycosylated; high-mannose.				
CC	-1- SIMILARITY: Belongs to the adenoviruses E19 family.				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				

the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

PIR: A03821; O6ADE.

InterPro: IPR009565; Adeno\_GPI9K.

Ptam; Adeno GP19K\_1.

Direct protein sequencing Early protein; Endoplasmic reticulum; Glycoprotein; Lectin; Mannose-binding; Membrane; Signal; Transmembrane; Viral immunoevasion.

SIGNAL 1 17

FT CHAIN 18 159 Early E3 18.5 kDa glycoprotein.

FT CHAIN 18 123 Lumenal (Potential).

FT TRANSMEM 124 144 Cytoplasmic (Potential).

FT TOPO\_DOM 145 159 Mediates endoplasmic reticulum retention

FT MOTIF 156 159 (By similarity).

FT CARBOHYD 29 29 N-linked (GlcNAc . . ) (Potential).

FT CARBOHYD 78 78 N-linked (GlcNAc . . ) (Potential).

FT DISULFID 28 45 FT DISULFID 39 100 C->S: Complete loss of binding to Tw1.3

FT MUTAGEN 28 28 C->A,S: 60% loss of binding to Tw1.3

FT MUTAGEN 39 39 C->A,S: 60% loss of binding to Tw1.3

FT MUTAGEN 45 45 C->S: Complete loss of binding to Tw1.3

FT MUTAGEN 100 100 C->S: 60% loss of binding to Tw1.3

FT MUTAGEN 118 118 C->A,S: No effect.

FT MUTAGEN 126 126 C->S: No effect.

FT MUTAGEN 139 139 C->S: No effect.

FT MUTAGEN 159 AA; 18438 MW; ED2519547E18ABBO CRC64;

SEQ SEQUENCE 159 AA; 18438 MW; ED2519547E18ABBO CRC64;

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

-|- DEVELOPMENTAL STAGE: Expressed at early period of virus infection.  
CC -|- DOMAIN: The luminal domain binds directly to the peptide-binding domain of class I molecules.

CC -|- PTM: Both disulfide bonds are absolutely critical for the interaction with MHC antigens (By similarity).

CC -|- PTM: N-glycosylation, high-mannose (By similarity).

CC -|- SIMILARITY: Belongs to the adenoviruses E19 family.

CC -|- This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -|- DR: Y16037; CAA75590\_1.; Genomic\_DNA.  
DR: InterPro: IPR006965; Adeno\_GPI9K.

DR: Pfam: PF04881; EndoTastic\_reticulum; Glycoprotein; Lectin;

DR: Kappa Protein; EndoTlastic membrane; Viral immunoevasion.

DR: SIGNAL 1 17  
FT SIGNAL 1 17  
FT CHAIN 18 159  
FT CHAIN 18 123  
FT TRANSMEM 18 123  
FT TRANSMEM 124 144  
FT TOPO\_DOM 145 159  
FT TOPO\_DOM 145 159  
FT MOTIF 156 159  
FT MOTIF 156 159  
FT CARBOHYD 18 159  
FT CARBOHYD 18 159  
FT CARBOHYD 78 78  
FT CARBOHYD 78 78  
FT DISULFID 28 45  
FT DISULFID 28 45  
FT DISULFID 39 100  
FT DISULFID 39 100  
SQ SEQUENCE 159 AA; 18438 MW; ED2519547E18ABBO CRC64;

Query Match 100.0%; Score 85; DB 1; Length 159;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18

Score 85; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGILALAAVCSAA 18

Db 1 MRYMILGILALAAVCSAA 18</p



Query Match	Score 51; DB 2; Length 179;	Pred. No. 17;	Gaps 0;	DR GO; GO:0005524; F:ATP binding; IEA.
Best Local Similarity	53.1%;			GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . . ; IEA.
Matches 8; Conservative	6; Mismatches 1; Indels 0;			GO; GO:0006810; F:ATPase activity, coupled to transmembrane m. . . ; IEA.
Qy	3 YMIGLGLAAVCSA 17 ::: :  : :  : Db	8 FVVGILALSAVQCA 22		DR InterPro; IPR001626; ABC_3.
RESULT 8				DR Pfam; PF00950; ABC_3; 1_
Q7QID4_ANOGA PRELIMINARY;	PRT;	208 AA.		KW Complete proteome; Transporter; Transport
ID Q7QID4;				SQ SEQUENCE 294 AA; BPP5B7C2998629D4 CRC64;
AC DT 01-MAR-2004 (TREMBLrel. 26, Created)				Query Match 60 0%; Score 51; DB 2; Length 294;
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)				Best Local Similarity 71.4%; Pred. No. 25;
DE ENSANGP00000013405 (Fragment); DE ORFNames=ENSANGC00000010916;				Mismatches 3; Indels 0; Gaps 0;
OS Anopheles gambiae STR. PEST.				
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;				
OC Anophelinae; Anophelidae.				
OX NCBI-TaxID:180454;				
RN [1]				
RP NUCLEOTIDE SEQUENCE.				
STRAIN=PEST;				
RG The Anopheles gambiae Sequence Committee;				
RT "Anopheles gambiae re-annotation.";				
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
[2]				
RP NUCLEOTIDE SEQUENCE.				
RC STRAIN=PEST;				
RG The Anopheles gambiae Sequence Committee;				
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.				
-!- CRUITION: The sequence shown here is derived from an				
CC CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is				
CC preliminary data.				
DR EMBL; AAAB0108807; EAA04053.2.; -; Genomic_DNA.				
FT NON_TER 208 208 AA;				
SQ SEQUENCE 208 AA; 22236 MW; OC842054742B1720 CRC64;				
Query Match 60 0%; Score 51; DB 2; Length 208;				
Best Local Similarity 44.4%; Pred. No. 19;				
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;				
Qy	1 MYRMICLGLAAVCSAA 18  : :  : :  : Db	1 MKYSLVAVLIAACSSA 18		
RESULT 9				
Q7U6KL_SYNPK SYNPK PRELIMINARY;	PRT;	294 AA.		
ID Q7U6KL_				
AC DT 01-OCT-2003 (TREMBLrel. 25, Created)				
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)				
DT 01-MAR-2004 (TREMBLrel. 25, Last annotation update)				
DE ABC transporter component, possibly Mn transport.				
GN OrderedLocusName=SYNW1337;				
OS Synechococcus sp. (strain WH8102).				
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.				
NCBI-TaxID=84588				
RN [1]				
RP NUCLEOTIDE SEQUENCE.				
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;				
RA Palenik B., Brahamsa B., Larimer F.W., Land M.L., Hauber L.,				
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,				
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.,				
RA "The genome of a motile marine Synechococcus.,"				
RL Nature 424:1037-1042 (2003); CAE07852.1; -; Genomic_DNA.				
DR EMBL; BX563692; CAE07852.1; -; Genomic_DNA.				
DR GO; GO:0016621; :integral to membrane; IEA.				
DR GO; GO:0016620; C:integral to membrane; IEA.				

Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 EMBL: CP000050; AY49880.1; -; Genomic\_DNA.  
 Hypothetical protein.  
 SEQUENCE 294 AA; 30273 MW; 6B95961AF717F215 CRC64;  
 SEQUENCE 294 AA; 30273 MW; 6B95961AF717F215 CRC64;  
 SEQUENCE 294 AA; 30273 MW; 6B95961AF717F215 CRC64;  
 SEQUENCE 294 AA; 30273 MW; 6B95961AF717F215 CRC64;

Query Match 57.6%; Score 49; DB 2; Length 29  
 Best Local Similarity 62.5%; Pred. No. 49;  
 Matches 10; Conservative 2; Mismatches 4; Indels 4;  
 Qy 1 MRWYIILGILLLAAVCS 16  
 ||||| :|||:  
 Db 1 MRWYIILGILLLAAVCS 16

RESULT 12  
 Q8PB18 XANCP  
 ID Q8PB18\_XANCP PRELIMINARY;  
 PRT; 294 AA.  
 AC Q8PB18;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DB Hypothetical protein XCC1308.  
 OrderdLocusName=XCC1308;  
 OS Xanthomonas campestris (pv. campestris).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonas.  
 OC Xanthomonadaceae; Xanthomonas.  
 NCBI\_TaxID=340;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE STRAINATAC2 33913 / NCGBB 528;  
 RC MEDLINE=22022145; Published=1024217; DOI=10.1038/117459a;  
 RX da Silva, A.C.R., Ferro J.A., Reinach F.C., Farah S., Faria C., Ferreira R.C.C., Gregorio G.C., Lemos E.G.M., Leite R.P., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.P. Jr., Alves L.M.C., do Amaral A.M., Bertolin Camargo L.E.A., Camarote G., Carnava F., Cardozo J.J., Ciapina L.P., Ciccarelli R.M.B., Coutinho L.I., Cursino-Silva, R.B.-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Gregorio G.C., Katsuyama A.M., Kishi I.T., Leite R.P., Lemos E.G.M., Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rodriguez J., Menck C.F.M., Miyaki Y., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira L.M., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza, Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Trindade dos Santos M., Truffi D., Tsai S.M., White F.P., Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens host specificities";  
 RT Nature 417:459-463 (2002).  
 RL EMBL: AE012230; AAM40506.1; -; Genomic DNA.  
 DR Complete proteome; Hypothetical protein.  
 KW SEQUENCE 294 AA; 30273 MW; 6B95961AF717F215 CRC64;  
 SEQUENCE 294 AA; 30273 MW; 6B95961AF717F215 CRC64;  
 SEQUENCE 294 AA; 30273 MW; 6B95961AF717F215 CRC64;

Query Match 57.6%; Score 49; DB 2; Length 29  
 Best Local Similarity 62.5%; Pred. No. 49;  
 Matches 10; Conservative 2; Mismatches 4; Indels 4;  
 Qy 1 MRWYIILGILLLAAVCS 16  
 ||||| :|||:  
 Db 1 MRWYIILGILLLAAVCS 16

RESULT 13  
 Q9V5Z3 DROMB  
 ID Q9V5Z3\_DROMB PRELIMINARY;  
 PRT; 181 AA.  
 AC Q9V5Z3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DB CGS027-Pa, isoform A (Cg9027-pb, isoform b) (LP09315p).  
 GN ORFnames=CG9027;  
 CC Drosophila melanogaster (fruit fly);  
 CC Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Drosophila; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota.





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Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	27	1	US-08-464-318-7
2	85	100.0	27	1	US-08-471-341-7
3	85	100.0	27	1	US-08-461-566-7
4	85	100.0	27	1	US-09-070-529-2
5	85	100.0	90	2	US-09-124-671-25
6	85	100.0	109	2	US-09-124-671-23
7	85	100.0	109	2	US-09-124-671-27
8	85	100.0	109	2	US-09-124-671-29
9	81	95.3	17	1	US-08-464-318-1
10	81	95.3	17	1	US-08-471-341-1
11	81	95.3	17	1	US-08-461-566-1
12	80	94.1	31	2	US-09-653-187-74
13	51	60.0	175	2	US-09-376-113-7
14	51	60.0	109	2	US-10-200-559-7
15	48	56.5	128	2	US-09-277-267-41350
16	48	56.5	128	2	US-09-270-767-5656
17	47	55.3	205	2	US-09-302-540-13846
18	47	55.3	305	2	US-09-489-039A-731
19	47	55.3	370	2	US-09-767-32759
20	47	55.3	370	2	US-09-270-6747976
21	46	54.1	157	2	US-09-250-991A-22612
22	45	52.9	485	2	US-09-302-14540
23	44	51.8	485	2	US-09-328-352-8210
24	43.5	51.2	195	2	US-09-252-991A-22429
25	43	50.6	208	2	US-09-248-796A-14596
26	43	50.6	319	2	US-10-028-051A-8
27	42	49.4	168	2	US-09-376-113-5

Total number of hits satisfying chosen parameters: 572060

Database : Issued Patents AA:\*

Post-processing: Minimum Match 100%  
 Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgcn2\_6/.ptodata/1/1aa/5\_COMB.pep:\*
- 2: /cgcn2\_6/.ptodata/1/1aa/6\_COMB.pep:\*
- 3: /cgcn2\_6/.ptodata/1/1aa/H\_COMB.pep:\*
- 4: /cgcn2\_6/.ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 5: /cgcn2\_6/.ptodata/1/1aa/RE\_COMB.pep:\*
- 6: /cgcn2\_6/.ptodata/1/1aa/backfilles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

## RESULT 1

US-08-44-318-7  
 Sequence 7, Application US/08464318  
 ; Patent No. 5733348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,  
 ; APPLICANT: STEVEN A. BENNINK, JACK R., BACIK, IGOR,  
 ; APPLICANT: YEWDELL, JONATHAN W  
 ; TITLE OF INVENTION: IMMUNOGENIC CHIMERICAS  
 ; COMPRISING NUCLEAR ACID SEQUENCES ENCODING  
 ; ENDOPLASMIC RETICULUM SIGNAL SEQUENCE  
 ; PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND  
 ; THEIR USES IN VACCINES AND DISEASE TREATMENTS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORGAN & FINNEGAN  
 ; STREET: 345 PARK AVENUE  
 ; CITY: NEW YORK  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10154  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WORD PERFECT 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/464-318  
 ; FILING DATE: 5-JUNE-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/032,902  
 ; FILING DATE: 17-MAR-1993  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: RICHARD W. BORK  
 ; REGISTRATION NUMBER: 3,6,459  
 ; REFERENCE/DOCKET NUMBER: 2026-4069US2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-755-4800  
 ; TELEFAX: 212-751-6849  
 ; TELEX: 422792  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 27 amino acid residues  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; US-08-464-318-7  
 ; Query Match 100.0%; Score 85; DB 1; Length 27;

Page 2

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RERESULT 2
US-08-471-341-7
; Sequence 7, Application US/08471341

Best Local Similarity 100.0%; Pred. No. 1.e-07; Mismatches 0; Indels 0; Gap
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gap
Qy 1 MRYMILGLLAAVCSAA 18
Dbb 1 MRYMILGLLAAVCSAA 18

RERESULT 3
US-08-471-341-7
; Sequence 7, Application US/08471341

Best Local Similarity 100.0%; Pred. No. 1.e-07; Length 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gap
Query Match
GENERAL INFORMATION:
APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
APPLICANT: BENNINK, JACK R., BACIK, IGOR,
APPLICANT: YENDELL, JONATHAN W.
TITLE OF INVENTION: IMMUNOGENIC CHIMMERS
TITLE OF INVENTION: COMBINING NUCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE
TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND
TITLE OF INVENTION: THEIR USES IN VACCINES AND DISEASE TREATMENTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,341
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,902
FILING DATE: 17-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4069
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acid residues
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

RERESULT 3
US-08-461-566-7
; Sequence 7, Application US/08461566

Best Local Similarity 100.0%; Pred. No. 1.e-07; Length 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gap
Query Match
GENERAL INFORMATION:
APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG,
APPLICANT: BENNINK, JACK R., BACIK, IGOR,
APPLICANT: YENDELL, JONATHAN W.

```

i OTHER INFORMATION: and beta-gal epitope  
us-09-070-629-2

Query Match Score 85; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 5

US-09-124-671-25  
Sequence 25, Application US/09124671A

Patent No. 6160088  
GENERAL INFORMATION:  
APPLICANT: Rothman, James

APPLICANT: Maynew, Mark  
APPLICANT: Hoe, Mee  
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488  
CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 25

LENGTH: 90  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: chimeric human pLB-KDEL

us-09-124-671-25

Query Match Score 85; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 6

US-09-124-671-23  
Sequence 23, Application US/09124671A

Patent No. 6160088  
GENERAL INFORMATION:  
APPLICANT: Rothman, James

APPLICANT: Maynew, Mark  
APPLICANT: Hoe, Mee  
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488  
CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 23

LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: chimeric human COMP-KDEL

us-09-124-671-23

Query Match Score 85; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 7

US-09-124-671-27  
Sequence 27, Application US/09124671A

Patent No. 6160088  
GENERAL INFORMATION:  
APPLICANT: Rothman, James

APPLICANT: Maynew, Mark  
APPLICANT: Hoe, Mee  
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488  
CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 27

LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: chimeric human TSP3-KDEL

us-09-124-671-27

Query Match Score 85; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 8

US-09-124-671-29  
Sequence 29, Application US/09124671A

Patent No. 6160088  
GENERAL INFORMATION:  
APPLICANT: Rothman, James

APPLICANT: Maynew, Mark  
APPLICANT: Hoe, Mee  
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488  
CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 29

LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: chimeric human TSP4-KDEL

us-09-124-671-29

Query Match Score 85; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLLAAAVCSAA 18  
Db 1 MRYMILGLLAAAVCSAA 18

RESULT 9

US-08-464-318-1  
Sequence 1, Application US/08464318

Patent No. 5733548  
GENERAL INFORMATION:  
APPLICANT: RESTIVO, NICHOLAS P.; ROSENBERG,

APPLICANT: STEVEN A.; BENNINK, JACK R.; BACIK, IGOR,

APPLICANT: YEWDELL, JONATHAN W

TITLE OF INVENTION: IMMUNOGENIC CHIMERIC

TITLE OF INVENTION: COMPRISING NUCLEIC ACID SEQUENCES ENCODING

TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND THEIR USES IN VACCINES AND DISEASE TREATMENTS

TITLE OF INVENTION: NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS: STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: U.S.A. ZIP: 10154

COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/0/8/464,318 FILING DATE: 5-JUNE-1995 CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/032,902 FILING DATE: 17-MAR-1993 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK REGISTRATION NUMBER: 36,459 REFERENCE DOCKET NUMBER: 2026-4069US2 TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800 TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acid residues TYPE: amino acid STRANDEDNESS: unknown

TOPOLOGY: unknown

US-08-464-318-1

Query Match Score 81; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 4.6e-07; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYYMIGLLAALAAVCSA 17  
Db 1 MRYYMIGLLAALAAVCSA 17

RESULT 10 US-08-471-341-1

Sequence 1, Application US/08461566

Patent No. 5846540

GENERAL INFORMATION:

APPLICANT: RESTIFO, NICHOLAS P., ROSENBERG, STEVEN A., BENNINK, JACK R., BACIK, IGOR, YEWDELL, JONATHAN W.

APPLICANT: STEVEN A., BENNINK, JACK R., BACIK, IGOR, YEWDELL, JONATHAN W.

TITLE OF INVENTION: IMMUNOGENIC CHIMERICAS COMPRISING NUCLEAR ACID SEQUENCES ENCODING ENDOPLASMIC RETICULUM SIGNAL SEQUENCE

TITLE OF INVENTION: ENDOPLASMIC RETICULUM SIGNAL SEQUENCE

TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND THEIR USES IN VACCINES AND DISEASE TREATMENTS

TITLE OF INVENTION: PEPTIDES AND AT LEAST ONE OTHER PEPTIDE, AND THEIR USES IN VACCINES AND DISEASE TREATMENTS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: U.S.A. ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,566 FILING DATE: 05-JUNE-1995 CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/032,902 FILING DATE: 17-MAR-1993 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK REGISTRATION NUMBER: 36,459 REFERENCE DOCKET NUMBER: 2026-4069US3 TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800 TELEFAX: 212-751-6849

TELELEX: 421792

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acid residues  
; TYPE: amino acid  
; STRANDBEDNESS: unknown  
; TOPOLOGY: unknown  
; US-08-461-566-1

Query Match 95.3%; Score 81; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Result 14  
US-10-200-659-7  
Db 1 MYRMLGLLAAVCSA 17

Result 12  
US-09-653-182-74  
Sequence 7, Application US/09653182  
; GENERAL INFORMATION:  
; Patent No. 6881825  
; APPLICANT: Paul D. Robbins  
; ATTORNEY: Zhibao Mi  
; APPLICANT: Raymond Frizzell  
; APPLICANT: Joseph C. Glorioso  
; APPLICANT: Andrea Gambotto  
; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR TRANSPORT  
; TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES  
; FILE REFERENCE: AP32573-A-A  
; CURRENT APPLICATION NUMBER: US/09/653,182  
; CURRENT FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/151,980  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: 60/188,944  
; PRIOR FILING DATE: 2000-03-13  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSEQ For Windows Version 3.0  
; SEQ ID NO: 74  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: random peptide library  
Result 15  
US-09-210-767-41350  
Sequence 41350, Application US/09270767  
; GENERAL INFORMATION:  
; Patent No. 6703491  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 6217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 41350  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: *Drosophila melanogaster*  
US-09-210-767-41350

Query Match 94.1%; Score 80; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RYMIGLGLLAAVCSA 18  
Db 15 RYMIGLGLLAAVCSA 31

Result 13  
US-09-376-113-7  
Sequence 7, Application US/09376113  
; Patent No. 6451992  
; GENERAL INFORMATION:  
; APPLICANT: CUPP, Eddie Wayne  
; TITLE OF INVENTION: Antithrombin Nucleotides and Proteins  
; FILE REFERENCE: 5721-10  
; CURRENT APPLICATION NUMBER: US/10/200,659  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/376,113  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 7  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Haematobia Irritans  
US-10-200-659-7

Query Match 60.0%; Score 51; DB 2; Length 175;  
Best Local Similarity 53.3%; Pred. No. 0.67%;  
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YMIGLGLLAAVCSA 17  
Db 4 FVVGIGLGLAAVCSA 18

Result 15  
US-09-210-767-41350  
Sequence 41350, Application US/09270767  
; GENERAL INFORMATION:  
; Patent No. 6703491  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 6217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 41350  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: *Drosophila melanogaster*  
US-09-210-767-41350

Query Match 56.5%; Score 48; DB 2; Length 128;  
Best Local Similarity 53.3%; Pred. No. 1.5%;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRYMIGLGLLAAVCSA 15  
Db 72 IRMVIVGTVALLVYC 86

Search completed: January 11, 2006, 00:10:38  
Job time : 23 secs

**This Page Blank (uspto)**

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## Om protein - protein search, using SW model

Run on: January 11, 2006, 00:09:44 ; Search time 61 Seconds  
 (without alignments)  
 123,294 Million cell updates/sec

Title: US-10-031-008-7  
 Perfect score: 85  
 Sequence: 1 MRYMTIGLLAAVCSAA 18

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqB, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA Main:  
 1: /cgpn2\_6/podata/1/pubpaas/us07\_pubcomb.pep:  
 2: /cgpn2\_6/podata/1/pubpaas/us08\_pubcomb.pep:  
 3: /cgpn2\_6/podata/1/pubpaas/us09\_pubcomb.pep:  
 4: /cgpn2\_6/podata/1/pubpaas/us10\_pubcomb.pep:  
 5: /cgpn2\_6/podata/1/pubpaas/us10b\_pubcomb.pep:  
 6: /cgpn2\_6/podata/1/pubpaas/us11\_pubcomb.pep:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	18	3 US-09-894-594-65	Sequence 65, Appl
2	85	100.0	18	3 US-09-894-594-70	Sequence 70, Appl
3	85	100.0	18	4 US-10-080-597-13	Sequence 13, Appl
4	85	100.0	27	5 US-10-848-520-2	Sequence 2, Appl
5	85	100.0	90	4 US-10-915-514-25	Sequence 25, Appl
6	85	100.0	90	5 US-10-873-594-25	Sequence 25, Appl
7	85	100.0	90	5 US-10-877-530-25	Sequence 23, Appl
8	85	100.0	109	4 US-10-815-514-23	Sequence 27, Appl
9	85	100.0	109	4 US-10-815-514-27	Sequence 29, Appl
10	85	100.0	109	4 US-10-815-514-29	Sequence 23, Appl
11	85	100.0	109	5 US-10-877-530-23	Sequence 27, Appl
12	85	100.0	109	5 US-10-877-530-29	Sequence 23, Appl
13	85	100.0	109	5 US-10-873-594-23	Sequence 23, Appl
14	85	100.0	109	5 US-10-873-594-27	Sequence 27, Appl
15	85	100.0	109	5 US-10-873-594-29	Sequence 29, Appl
16	85	100.0	109	5 US-10-873-594-29	Sequence 2, Appl
17	82	96.5	26	4 US-10-331-163-2	Sequence 2, Appl
18	80	94.1	31	4 US-10-715-869-74	Sequence 74, Appl
19	80	94.1	31	5 US-10-366-93-74	Sequence 74, Appl
20	80	94.1	31	5 US-10-926-93-74	Sequence 74, Appl
21	51	60.0	175	4 US-10-20-659-7	Sequence 7, Appl
22	48	56.5	179	6 US-11-097-143-19317	Sequence 28,680, A
23	48	56.5	181	6 US-11-097-143-24680	Sequence 8319, Ap
24	46	54.1	140	4 US-10-156-761-8319	Sequence 216633,
25	46	54.1	148	4 US-10-424-599-216653	Sequence 74, Appl
26	46	54.1	5175	4 US-10-120-801-74	Sequence 6859, Ap
27	46	54.1	5175	4 US-10-369-493-6859	Sequence 240570,

## ALIGNMENTS

RESULT: 1  
 US-09-894-594-65  
 ; Sequence 65, Application US/09894594  
 ; Publication No. US20030017497A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieber-Emmons, Thomas  
 ; APPLICANT: Werner, David B.  
 ; APPLICANT: Monzavi-Karbassi, Behjatollah  
 ; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encoded by Genes  
 ; FILE REFERENCE: UPN-3984  
 ; CURRENT APPLICATION NUMBER: US/09-894-594  
 ; CURRENT FILING DATE: 2001-06-28  
 ; PRIORITY APPLICATION NUMBER: 09/601,558  
 ; PRIORITY FILING DATE: 2000-11-07  
 ; PRIORITY APPLICATION NUMBER: PCT/US99/024405  
 ; PRIORITY FILING DATE: 1999-02-04  
 ; PRIORITY APPLICATION NUMBER: 60/073,690  
 ; PRIORITY FILING DATE: 1998-02-04  
 ; PRIORITY APPLICATION NUMBER: 60/214,517  
 ; PRIORITY FILING DATE: 2000-06-28  
 ; NUMBER OF SEQ ID NO: 70  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 65  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Novel Sequence  
 US-09-894-594-65

Query Match Score 100.0%; Best local Similarity 100.0%; Matches 18; DB 3; Length 18;  
 保守型 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMLGLLAAVCSAA 18  
 Db 1 MRYMLGLLAAVCSAA 18

RESULT: 2  
 US-09-894-594-70  
 ; Sequence 70, Application US/09894594  
 ; Publication No. US20030017497A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieber-Emmons, Thomas  
 ; APPLICANT: Werner, David B.  
 ; APPLICANT: Monzavi-Karbassi, Behjatollah  
 ; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encoded by Genes

TITLE OF INVENTION: Same  
FILE REFERENCE: UBN-3984  
CURRENT APPLICATION NUMBER: US/09/894,594  
CURRENT FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: 09/601,558  
PRIOR FILING DATE: 1998-11-07  
PRIOR APPLICATION NUMBER: PCT/US99/02405  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: 60/073,690  
PRIOR FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: 60/214,517  
PRIOR FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 70  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Novel Sequence  
US-09-894-594-70

Query Match Score 85; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 3  
US-10-080-797-13  
Sequence 13, Application US/10080797  
Publication No. US20020183253A1  
GENERAL INFORMATION:  
APPLICANT: Campochiaro, Peter A.  
APPLICANT: Dixon, Katherine H.  
APPLICANT: Brazzell, Romulus K.  
TITLE OF INVENTION: METHOD FOR TREATING OCULAR  
TITLE OF INVENTION: NEOVASCULARIZATION  
FILE REFERENCE: 4-1881A  
CURRENT APPLICATION NUMBER: US/10/080,797  
CURRENT FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSEQ For Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Adenovirus  
US-10-080-797-13

Query Match Score 85; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 4  
US-10-848-620-2  
Sequence 2, Application US/10848620  
Publication No. US2004025273A1  
GENERAL INFORMATION:  
APPLICANT: Palise, P.  
APPLICANT: Garcia-Gastre, A.  
APPLICANT: Restifo, N.  
TITLE OF INVENTION: RECOMBINANT INFLUENZA VIRUSES EXPRESSING  
TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGENS AS ANTI TUMOR AGENTS  
FILE REFERENCE: 6923-071

CURRENT APPLICATION NUMBER: US/10/848,620  
CURRENT FILING DATE: 2004-05-17  
PRIOR APPLICATION NUMBER: US/09/070,629  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/045,176  
PRIOR FILING DATE: 1998-04-30  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 27  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Leader peptide  
US-10-848-620-2

Query Match Score 85; DB 5; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 5  
US-10-815-514-25  
Sequence 25, Application US/10815514  
Publication No. US2004204361A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James  
APPLICANT: Mayhew, Mark  
APPLICANT: Hoe, Mee  
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
FILE REFERENCE: 31488  
CURRENT APPLICATION NUMBER: US/10/815,514  
CURRENT FILING DATE: 2004-03-31  
PRIOR APPLICATION NUMBER: US/09/696,872  
PRIOR FILING DATE: 2000-10-26  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSEQ For Windows Version 3.0  
SEQ ID NO 25  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chimeric human PLB-KDEL  
US-10-815-514-25

Query Match Score 85; DB 4; Length 90;  
Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 6  
US-10-077-930-25  
Sequence 25, Application US/10877930  
Publication No. US2004035123A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James  
APPLICANT: Mayhew, Mark  
APPLICANT: Hoe, Mee  
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
FILE REFERENCE: 31488  
CURRENT APPLICATION NUMBER: US/10/877,930  
CURRENT FILING DATE: 2004-06-25  
PRIOR APPLICATION NUMBER: US/09/696,070  
PRIOR FILING DATE: 2000-10-25

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; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-977-930-25

Query Match 100.0%; Score 85; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: DOMAIN
Qy 1 MRYMILGLLAAVCSAA 18
Db 1 MRYMILGLLAAVCSAA 18

RESULT 7
US-10-873-594-25
; Sequence 25, Application US/10873594
; Publication No. US20050095667A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-1-1 065360_0152
; CURRENT APPLICATION NUMBER: US/10/873,594
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/09/800,358
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/696,070
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/124,671
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 25
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric KDEL receptor inhibitor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) ..(20)
; OTHER INFORMATION: Cleavable leader/signal peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (10) ..(36)
; OTHER INFORMATION: human PLB pentamerization domain
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (13) ..(13)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (18) ..(18)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (21) ..(21)
; OTHER INFORMATION: Critical for pentamer formation

; FEATURE; NAME/KEY: BINDING
; LOCATION: (24) ..(24)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (28) ..(28)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (31) ..(31)
; OTHER INFORMATION: Critical for pentamer formation
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (37) ..(60)
; OTHER INFORMATION: Camel IgG linker domain
US-10-873-594-25

Query Match 100.0%; Score 85; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: DOMAIN
Qy 1 MRYMILGLLAAVCSAA 18
Db 1 MRYMILGLLAAVCSAA 18

RESULT 8
US-10-815-514-23
; Sequence 23, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 23
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human COMP-KDEL
US-10-815-514-23

Query Match 100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: DOMAIN
Qy 1 MRYMILGLLAAVCSAA 18
Db 1 MRYMILGLLAAVCSAA 18

RESULT 9
US-10-815-514-27
; Sequence 27, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human COMP-KDEL
US-10-815-514-27

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; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP3-KDEL
US-10-815-514-27

Query Match 100.0%; Score 85; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
RESULT 12
US-10-877-930-27
; Sequence 27, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP3-KDEL
US-10-877-930-27

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
RESULT 13
US-10-877-930-29
; Sequence 29, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP4-KDEL
US-10-877-930-29

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
RESULT 14
US-10-877-930-30
; Sequence 30, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP4-KDEL
US-10-877-930-30

Query Match 100.0%; Score 85; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 5e-05; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
RESULT 15
US-10-877-930-31
; Sequence 31, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human TSP4-KDEL
US-10-877-930-31

```

Qy 1 MRYMILGLALAAVCSAA 18  
 Db 1 MRYMILGLALAAVCSAA 18

RESULT 14  
 US-10-873-594-23  
 Sequence 23, Application US/10873594  
 Publication No. US20050095667A1  
 GENERAL INFORMATION:  
 APPLICANT: Rothman, James  
 APPLICANT: Maynew, Mark  
 APPLICANT: Hoe, Mee  
 TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
 FILE REFERENCE: A31488-1-I 065360.0152  
 CURRENT APPLICATION NUMBER: US/10/873..594  
 CURRENT FILING DATE: 2004-06-21  
 PRIOR APPLICATION NUMBER: US/09/800,358  
 PRIOR FILING DATE: 2001-03-05  
 PRIOR APPLICATION NUMBER: 09/696,070  
 PRIOR FILING DATE: 2000-10-25  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 23  
 LENGTH: 109  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Chimeric KDEL receptor inhibitor  
 NAME/KEY: SIGNAL  
 LOCATION: (1)..(20)  
 OTHER INFORMATION: Cleavable leader/signal peptide  
 FEATURE:  
 OTHER INFORMATION: Chimeric KDEL receptor inhibitor  
 NAME/KEY: SIGNAL  
 LOCATION: (1)..(20)  
 OTHER INFORMATION: Cleavable leader/signal peptide  
 FEATURE:  
 OTHER INFORMATION: Chimeric KDEL receptor inhibitor  
 NAME/KEY: SIGNAL  
 LOCATION: (1)..(20)  
 OTHER INFORMATION: Cleavable leader/signal peptide  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (1)..(3)  
 OTHER INFORMATION: Linker  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (10)..(55)  
 OTHER INFORMATION: human TSP3 trimerization domain  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (6)..(9)  
 OTHER INFORMATION: The sub-sequence GDCC  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (10)..(79)  
 OTHER INFORMATION: human TSP3 trimerization domain  
 FEATURE:  
 NAME/KEY: DOMAIN  
 LOCATION: (56)..(95)  
 OTHER INFORMATION: Camel IgG linker domain  
 US-10-873-594-27

Query Match 100.0%; Score 85; DB 5; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 5e-05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYMILGLALAAVCSAA 18  
 Db 1 MRYMILGLALAAVCSAA 18

Search completed: January 11, 2006, 00:19:38  
 Job time : 62 secs

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RESULT 15  
 US-10-873-594-27  
 Sequence 27, Application US/10873594  
 Publication No. US20050095667A1  
 GENERAL INFORMATION:  
 APPLICANT: Rothman, James  
 APPLICANT: Maynew, Mark  
 APPLICANT: Hoe, Mee  
 TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
 FILE REFERENCE: A31488-1-I 065360.0152

Qy 1 MRYMILGLALAAVCSAA 18  
 Db 1 MRYMILGLALAAVCSAA 18

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OM protein - protein search, using SW model

Run on: January 11, 2006, 00:10:09 ; Search time 8 Seconds  
(without alignments)

19.111 Million cell updates/sec

Title: US-10-031-008-7

Perfect score: 65

Sequence: 1 MRYMILGLALAAVCSAA 18

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:  
 1: /cgcn2\_6\_ptodata/1/pubaa/us08\_new\_pub.pep\*  
 2: /cgcn2\_6\_ptodata/1/pubaa/us06\_new\_pub.pep\*  
 3: /cgcn2\_6\_ptodata/1/pubaa/us07\_new\_pub.pep\*  
 4: /cgcn2\_6\_ptodata/1/pubaa/pct\_new\_pub.pep\*  
 5: /cgcn2\_6\_ptodata/1/pubaa/us09\_new\_pub.pep\*  
 6: /cgcn2\_6\_ptodata/1/pubaa/us10\_new\_pub.pep\*  
 7: /cgcn2\_6\_ptodata/1/pubaa/us11\_new\_pub.pep\*  
 8: /cgcn2\_6\_ptodata/1/pubaa/us01\_new\_pub.pep\*  
 \* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	50.6	319	7	US-11-184-005-8
2	41	48.2	152	7	US-11-184-005-2
3	40	47.1	325	7	US-11-184-005-4
4	40	47.1	824	6	US-10-821-034-1008
5	39	45.9	74	7	US-11-000-463-819
6	39	45.9	74	7	US-11-000-463-820
7	39	45.9	331	7	US-11-143-980-57
8	39	45.9	502	7	US-11-102-240-158
9	39	45.9	1061	7	US-11-000-463-347
10	39	45.9	1091	7	US-11-000-663-348
11	38	44.7	163	7	US-11-102-240-160
12	38	44.7	618	7	US-11-078-735-18
13	37.5	44.1	303	6	US-10-821-334-1661
14	37	43.5	243	6	US-10-878-556A-118
15	37	43.5	243	6	US-10-467-657-1286
16	37	43.5	861	6	US-11-186-284-157
17	36	42.4	143	7	US-11-186-284-159
18	36	42.4	350	6	US-10-878-528-132
19	36	42.4	390	6	US-10-131-86A-338
20	36	42.4	548	6	US-10-055-977-120
21	36	42.4	675	6	US-10-055-977-117
22	36	42.4	146	6	US-10-055-977-317
23	35	41.2	158	7	US-11-097-622-10
24	35	41.2	181	7	US-11-000-463-409

RESULT 1  
US-11-184-005-8

; Sequence 8 Application US/11184005  
; Publication No. US20050256052A1  
; GENERAL INFORMATION:  
; APPLICANT: Layten, Frank P.  
; APPLICANT: Moes, Malcolm JR.  
; APPLICANT: Hoang, Bang  
; APPLICANT: Wang, Shouwen  
; TITLE OF INVENTION: MODULATING TISSUE GROWTH USING FRZB PROTEIN  
; FILE REFERENCE: NTH133\_1CPC3  
; CURRENT APPLICATION NUMBER: US/11/184,005  
; CURRENT FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: US 10/028051  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US 08/822333  
; PRIOR FILING DATE: 1997-03-20  
; PRIOR APPLICATION NUMBER: US 08/729,452  
; PRIOR FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 319  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
; US-11-184-005-8

Qy 4 MILLAGLLAAVC 15  
 :: |||||: |  
 Db 10 LLAGLALLAAC 21

RESULT 2  
US/11/005  
; Sequence 31 Application US/11020772  
; Publication No. US20050256043A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig, Linda B.  
; TITLE OF INVENTION: HIV Antisense Proteins  
; FILE REFERENCE: 25125.0001  
; CURRENT APPLICATION NUMBER: US/11/020,772

CURRENT FILING DATE: 2004-12-23  
 PRIORITY APPLICATION NUMBER: US 09/249,542  
 PRIOR FILING DATE: 1999-02-12  
 PRIORITY APPLICATION NUMBER: US 60/074,640  
 PRIOR FILING DATE: 1998-02-13  
 PRIORITY APPLICATION NUMBER: US 08/853,703  
 PRIOR FILING DATE: 1997-05-09  
 NUMBER OF SEQ ID NOS: 36  
 SEQ ID NO: 31  
 LENGTH: 152  
 TYPE: PRT  
 OTHER INFORMATION: HIV antisense HAP protein translated from AUG start; requires -1  
 OTHER INFORMATION: HIV antisense HAP protein translated from AUG start; requires -1  
 US 11/020,772-31

Query Match 48.2%; Score 41; DB 7; Length 152;  
 Best Local Similarity 46.7%; Prod. No. 3.5;  
 Matches 7; Conservative 6; Mismatches 2; Indels 0;  
 Gaps 0;  
 Qy 4 MIGLLAAAVCSAA 18  
 Db 102 MLVGIWSLALVCNSA 116

RESULT 3  
 US-11-184-005-2  
 Sequence 2, Application US/11184005  
 Publication No. US20050256052A1  
 GENERAL INFORMATION:  
 APPLICANT: Layten, Frank P.  
 APPLICANT: Moos, Malcolm JR.  
 APPLICANT: Hoang, Bang  
 APPLICANT: Wang, Shouwen  
 TITLE OF INVENTION: METHOD OF MODULATING TISSUE  
 FILE REFERENCE: NIH133\_1CPC3  
 CURRENT APPLICATION NUMBER: US/11/184,005  
 CURRENT FILING DATE: 2005-07-18  
 PRIOR APPLICATION NUMBER: US 10/028051  
 PRIOR FILING DATE: 2001-12-19  
 PRIOR APPLICATION NUMBER: US 08/822333  
 PRIOR FILING DATE: 1997-03-20  
 PRIOR APPLICATION NUMBER: US 08/729,452  
 PRIOR FILING DATE: 1996-10-11  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 2  
 LENGTH: 325  
 TYPE: PRT  
 ORGANISM: Bos taurus  
 US-11-184-005-2

FILE REFERENCE: NIH133\_1CPC3  
 CURRENT APPLICATION NUMBER: US/11/184,005  
 CURRENT FILING DATE: 2005-07-18  
 PRIOR APPLICATION NUMBER: US 10/028051  
 PRIOR FILING DATE: 2001-12-19  
 PRIOR APPLICATION NUMBER: US 08/822333  
 PRIOR FILING DATE: 1997-03-20  
 PRIOR APPLICATION NUMBER: US 08/729,452  
 PRIOR FILING DATE: 1996-10-11  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 4  
 LENGTH: 325  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-184-005-4

Query Match 47.1%; Score 40; DB 7; Length 325;  
 Best Local Similarity 88.9%; Prod. No. 11;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0;  
 Gaps 0;  
 Qy 7 GLLLAAAVC 15  
 Db 15 GLLLAAALC 23

RESULT 5  
 US-10-821-234-1008  
 Sequence 1008, Application US/10821234  
 Publication No. US2005025514A1  
 GENERAL INFORMATION:  
 APPLICANT: Labat, Ivan  
 APPLICANT: Stach-Crain, Birgit  
 APPLICANT: Andarmani, Susan  
 APPLICANT: Tang, Y. Tom  
 TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 FILE REFERENCE: 821A  
 CURRENT APPLICATION NUMBER: US/10/821,234  
 CURRENT FILING DATE: 2004-04-07  
 PRIOR APPLICATION NUMBER: US 60/462,047  
 PRIOR FILING DATE: 2003-04-07  
 NUMBER OF SEQ ID NOS: 1704  
 SOFTWARE: pt SEQ\_genes Version 1.0  
 SEQ ID NO: 1008  
 LENGTH: 824  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-821-234-1008

Query Match 47.1%; Score 40; DB 7; Length 824;

Best Local Similarity 75.0%; Prod. No. 30;  
 Matches 9; Conservative 2; Mismatches 1;  
 Indels 0; Gaps 0;

Qy 6 IGLLLAAVCSA 17  
 Db 55 IGLLLAAVAAA 66

RESULT 6  
 US-11-000-463-819  
 Sequence 819, Application US/110000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng

RESULT 4  
 US-11-184-005-4  
 Sequence 4, Application US/11184005  
 Publication No. US20050256052A1  
 GENERAL INFORMATION:  
 APPLICANT: Layten, Frank P.  
 APPLICANT: Moos, Malcolm JR.  
 APPLICANT: Hoang, Bang  
 APPLICANT: Wang, Shouwen  
 TITLE OF INVENTION: METHOD OF MODULATING TISSUE  
 FILE REFERENCE: NIH133\_1CPC3

APPLICANT: Drmanac, Radoje T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785CIPACN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 PRIOR FILING DATE: 2000-09-15  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 819  
 LENGTH: 74  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-819

Query Match Score 39; DB 7; Length 74;  
 Best Local Similarity 50.0%; Pred. No. 3.4%;  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MILGLLAAAVC 15  
 Db 1 MVGVAAARLC 12

RESULT 7  
 US-11-000-463-820  
 Sequence 820, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhwei  
 APPLICANT: Wenzman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Drmanac, Radoje T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 820

LENGTH: 74  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-820

Query Match Score 39; DB 7; Length 74;  
 Best Local Similarity 50.0%; Pred. No. 3.4%;  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MILGLLAAAVC 15  
 Db 1 MVGVAAARLC 12

RESULT 8  
 US-11-143-980-57  
 Sequence 57, Application US/1143980  
 Publication No. US20050272133A1  
 GENERAL INFORMATION:  
 APPLICANT: He, Min  
 APPLICANT: Huctul, John  
 APPLICANT: Hultli, Bradley A.  
 APPLICANT: Wagenaar, Melissa M.  
 APPLICANT: Graziani, Edmund  
 APPLICANT: Summers, Mia  
 APPLICANT: Kulowski, Karrey  
 APPLICANT: Pong, Kevin  
 TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex  
 FILE REFERENCE: AM-101426US  
 CURRENT APPLICATION NUMBER: US/11/143,980  
 CURRENT FILING DATE: 2005-06-03  
 PRIOR APPLICATION NUMBER: US 60/664,483  
 PRIOR FILING DATE: 2005-03-23  
 PRIOR APPLICATION NUMBER: US 60/576,895  
 PRIOR FILING DATE: 2004-06-03  
 NUMBER OF SEQ ID NOS: 72  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO: 57

LENGTH: 331  
 TYPE: PRT  
 ORGANISM: Streptomyces sp.  
 US-11-143-980-57

Query Match Score 39; DB 7; Length 331;  
 Best Local Similarity 56.2%; Pred. No. 16%;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 YMIGLLAAAVCSAA 18  
 Db 192 YLGNGLGLAAVCAS 207

RESULT 9  
 US-11-102-240-158  
 Sequence 158, Application US/11102240  
 Publication No. US2005026647A1  
 GENERAL INFORMATION:  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Goowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Antibodies to Polypeptides Encoded by a Nucleic Acid Underexpressed  
 FILE REFERENCE: P3230R1C106C  
 CURRENT APPLICATION NUMBER: US/11/102,240  
 CURRENT FILING DATE: 2005-04-08  
 PRIOR APPLICATION NUMBER: 10/063662  
 PRIOR FILING DATE: 2002-05-07  
 PRIOR APPLICATION NUMBER: 10/006867  
 PRIOR FILING DATE: 2001-12-06  
 PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: 60/170262  
 SEQ ID NO: 158  
 LENGTH: 502  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-11-102-240-158

Query Match 45.9%; Score 39; DB 7; Length 502;  
 Best Local Similarity 60.0%; Pred. No. 26;  
 Matches 3; Indels 0; Gaps 0;

Qy 4 MIGGLAAAVCSAA 18  
 Db 1 MSLVLLSIALCRSA 15

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**RESULT 10**  
 Sequence 347, Application US/11000463  
 Publication No. US20050266423A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Zhou, Ping  
 APPLICANT: Cao, Yi-Cheng  
 APPLICANT: Dumanac, Radoe T.  
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 785C1P4CN  
 CURRENT APPLICATION NUMBER: US/11/000,463  
 CURRENT FILING DATE: 2004-11-29  
 PRIOR APPLICATION NUMBER: 10/291,265  
 PRIOR FILING DATE: 2002-11-08  
 PRIOR APPLICATION NUMBER: PCT/US01/02623  
 PRIOR FILING DATE: 2001-01-25  
 PRIOR APPLICATION NUMBER: 09/922,279  
 PRIOR FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: 09/491,404  
 PRIOR FILING DATE: 2000-01-25  
 PRIOR APPLICATION NUMBER: 09/617,746  
 PRIOR FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/631,451  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: 09/633,870  
 PRIOR FILING DATE: 2000-09-15  
 NUMBER OF SEQ ID NOS: 944  
 SOFTWARE: Fast-SEQ for Windows Version 3.0  
 SEQ ID NO: 348  
 LENGTH: 1091  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-348

Query Match 45.9%; Score 39; DB 7; Length 1091;  
 Best Local Similarity 50.0%; Pred. No. 58;  
 Matches 6; Indels 0; Gaps 0;

Qy 4 MILGILAAAVC 15  
 Db 1018 MVVGIVAAAALC 1029

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**RESULT 12**  
 Sequence 160, Application US/110102240  
 Publication No. US2005026647A1  
 GENERAL INFORMATION:  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurley, Austin L.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS:  
 FILE REFERENCE: P3230RLC106C  
 CURRENT APPLICATION NUMBER: US/11/102,240  
 CURRENT FILING DATE: 2005-04-08  
 PRIOR APPLICATION NUMBER: 10/063,662  
 PRIOR FILING DATE: 2002-05-07  
 PRIOR APPLICATION NUMBER: 10/006867  
 PRIOR FILING DATE: 2001-12-06  
 PRIOR APPLICATION NUMBER: PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: 60/170262  
 PRIOR FILING DATE: 199-12-09  
 NUMBER OF SEQ ID NOS: 170  
 SEQ ID NO: 160

Query Match 45.9%; Score 39; DB 7; Length 1061;  
 Best Local Similarity 50.0%; Pred. No. 56;  
 Matches 6; Indels 0; Gaps 0;

Qy 4 MIGGLAAAVC 15  
 Db 988 MVVGIVAAAALC 999

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**RESULT 11**  
 Sequence 348, Application US/11000463  
 Publication No. US-11-000-463-348  
 LENGTH: 1061  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-000-463-347

LENGTH: 163  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-11-102-240-160

Query Match 44.7%; Score 38; DB 7; Length 163;  
 Best Local Similarity 38.9%; Pred. No. 11;  
 Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRYMILGLALAACCSA 18  
 ::|:| :| | :| |:  
 Db 12 VRYLILSLGLAFLESEA 29

RESULT 13

US-11-018-735-18

Sequence 18. Application US/11078735  
Publication No. US20050261477A1

GENERAL INFORMATION:

APPLICANT: CHAMPION, BRIAN ROBERT  
LENNARD, ANDREW CHRISTOPHER  
MCKENZIE, GRAHAME JAMES  
TUGAL, TAMARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS

TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS

FILE REFERENCE: 674525-2019

CURRENT APPLICATION NUMBER: US/11/078,735  
CURRENT FILING DATE: 2005-03-10  
PRIOR APPLICATION NUMBER: PCT/GB03/03908  
PRIOR FILING DATE: 2003-09-09  
PRIOR APPLICATION NUMBER: PCT/GB03/03285  
PRIOR FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: PCT/GB03/01525  
PRIOR FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: GB 0300234.2  
PRIOR FILING DATE: 2003-01-07  
PRIOR APPLICATION NUMBER: PCT/GB02/05137  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: PCT/GB02/05133  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: GB 0220912.0  
PRIOR FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: GB 0220913.8  
PRIOR FILING DATE: 2002-09-10  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO: 18  
LENGTH: 618  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-078-735-18

Query Match 44.1%; Score 37.5; DB 7; Length 618;  
 Best Local Similarity 50.0%; Pred. No. 56;  
 Matches 10; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 RYMI--LGILALAAVCSSA 18  
 ::|:| | | | | | |:  
 Db 4 90 RYLPPGLLVAAGVAGAA 509

RESULT 14

US-10-821-234-1661

Sequence 1661, Application US/10821234  
Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan  
Stache-Crain, Birgit  
Andamani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234

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Search completed: January 11, 2006, 00:19:57  
Job time : 9 secs

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